RAW SEQUENCE LISTING

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Application Serial Number: _____ 10/655,915 A _____
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IFW16

RAW SEQUENCE LISTING   DATE: 08/17/2006
PATENT APPLICATION: US/10/655,915A   TIME: 10:46:16

Input Set : A:\960296.99080 - SEQ ID LISTING.txt
Output Set: N:\CRF4\08172006\J655915A.raw

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 3 <110> APPLICANT: Attie, Alan D
 4         Stoehr, Jonathan P
 5         Schueler, Kathryn L
 6         Clee, Susanne M
 8 <120> TITLE OF INVENTION: GENES ASSOCIATED WITH TYPE II DIABETES
10 <130> FILE REFERENCE: 960296.99080
12 <140> CURRENT APPLICATION NUMBER: 10/655,915A
13 <141> CURRENT FILING DATE: 2003-09-05
15 <150> PRIOR APPLICATION NUMBER: US 60/409,525
16 <151> PRIOR FILING DATE: 2002-09-09
18 <160> NUMBER OF SEQ ID NOS: 14
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 5757
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
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30 <222> LOCATION: (228)..(3893)
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37 acacacacgc tcgctcgctc gccggcgcgc gcacacccccc cgcgccggac ccgcacctcg    180
39 gcgggcgcca cacactcggc agcccgagcc gcggtagccg cagcgggg atg gag gcg      236
40                                                      Met Glu Ala
41                                                       1
43 gcg cgc acg gag cgc ccc gca ggc agg ccg ggg gcg ccg ctt gtc cgg     284
44 Ala Arg Thr Glu Arg Pro Ala Gly Arg Pro Gly Ala Pro Leu Val Arg
45     5                  10                  15
47 acg ggg ctc cta ctc ttg tcg acg tgg gtc ctg gcc ggc gcc gag atc     332
48 Thr Gly Leu Leu Leu Leu Ser Thr Trp Val Leu Ala Gly Ala Glu Ile
49 20                  25                  30                  35
51 act tgg gac gcg aca ggc ggt ccc gga cgc ccg gcg gcc ccg gct tcg     380
52 Thr Trp Asp Ala Thr Gly Gly Pro Gly Arg Pro Ala Ala Pro Ala Ser
53                  40                  45                  50
55 cgg cca ccg gcg ttg tct cca ctc tcg ccg cgg gca gtg gcc agc cag     428
56 Arg Pro Pro Ala Leu Ser Pro Leu Ser Pro Arg Ala Val Ala Ser Gln
57              55                  60                  65
59 tgg ccg gag gag ctg gcg tcg gcg cgg aga gcc gcc gtg ctg ggg cgc     476
60 Trp Pro Glu Glu Leu Ala Ser Ala Arg Arg Ala Ala Val Leu Gly Arg
61          70                  75                  80
63 cgg gcc gga cca gag ctg ctg ccc cag cag ggc ggc ggc aga ggc ggt     524
64 Arg Ala Gly Pro Glu Leu Leu Pro Gln Gln Gly Gly Gly Arg Gly Gly
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65      85                    90                   95
67 gag atg cag gtg gaa gcc gga ggg aca tca ccg gca ggc gag cgg cgg        572
68 Glu Met Gln Val Glu Ala Gly Gly Thr Ser Pro Ala Gly Glu Arg Arg
69 100                  105                  110                  115
71 ggc cgg ggc atc cca gct cct gcc aag ctt ggc ggc gcg agg agg agt        620
72 Gly Arg Gly Ile Pro Ala Pro Ala Lys Leu Gly Gly Ala Arg Arg Ser
73                  120                  125                  130
75 cgc cgg gcg cag ccc cca atc acc cag gaa cgc ggg gac gcc tgg gcc        668
76 Arg Arg Ala Gln Pro Pro Ile Thr Gln Glu Arg Gly Asp Ala Trp Ala
77              135                  140                  145
79 act gct ccg gcc gat ggt tcc aga gga agc cgt ccc ctt gct aag ggt        716
80 Thr Ala Pro Ala Asp Gly Ser Arg Gly Ser Arg Pro Leu Ala Lys Gly
81          150                  155                  160
83 tcc cgg gag gag gtg aag gcg ccg cgg gct ggg ggg tcg gcg gct gaa        764
84 Ser Arg Glu Glu Val Lys Ala Pro Arg Ala Gly Gly Ser Ala Ala Glu
85      165                  170                  175
87 gac ctc cgg ctg ccc agc acc tcc ttc gcg ctg acc ggg gac tcg gcc        812
88 Asp Leu Arg Leu Pro Ser Thr Ser Phe Ala Leu Thr Gly Asp Ser Ala
89 180                  185                  190                  195
91 cac aac caa gcc atg gtg cac tgg tcg gga cac aac agc agc gtc ata        860
92 His Asn Gln Ala Met Val His Trp Ser Gly His Asn Ser Ser Val Ile
93                  200                  205                  210
95 ctt atc ctg acg aag ctg tat gac ttc aac ctg ggc agc gtg act gag        908
96 Leu Ile Leu Thr Lys Leu Tyr Asp Phe Asn Leu Gly Ser Val Thr Glu
97              215                  220                  225
99 agt tca cta tgg agg tcg aca gat tat ggc acc acc tat gaa aag ctg        956
100 Ser Ser Leu Trp Arg Ser Thr Asp Tyr Gly Thr Thr Tyr Glu Lys Leu
101          230                  235                  240
103 aat gac aaa gtg ggt ttg aag act gtc ctc agt tac ctc tat gtc aat       1004
104 Asn Asp Lys Val Gly Leu Lys Thr Val Leu Ser Tyr Leu Tyr Val Asn
105      245                  250                  255
107 cca acc aac aaa agg aag att atg ctt ctc agt gat cct gag atg gag       1052
108 Pro Thr Asn Lys Arg Lys Ile Met Leu Leu Ser Asp Pro Glu Met Glu
109 260                  265                  270                  275
111 agc agc ata ttg atc agc tca gac gaa ggg gcg acc tat cag aag tat       1100
112 Ser Ser Ile Leu Ile Ser Ser Asp Glu Gly Ala Thr Tyr Gln Lys Tyr
113                  280                  285                  290
115 cgg ctc acc ttc tat atc cag agc ctg ctc ttt cat ccc aag caa gag       1148
116 Arg Leu Thr Phe Tyr Ile Gln Ser Leu Leu Phe His Pro Lys Gln Glu
117              295                  300                  305
119 gac tgg gtg ctg gcc tac agt ttg gat caa aag ctc tac agc tcc atg       1196
120 Asp Trp Val Leu Ala Tyr Ser Leu Asp Gln Lys Leu Tyr Ser Ser Met
121          310                  315                  320
123 gac ttt gga aga cgg tgg caa ctc atg cat gaa cgc atc aca ccc aac       1244
124 Asp Phe Gly Arg Arg Trp Gln Leu Met His Glu Arg Ile Thr Pro Asn
125      325                  330                  335
127 agg ttt tat tgg tcg gtg gcc gga ttg gat aag gag gcg gac ctg gtg       1292
128 Arg Phe Tyr Trp Ser Val Ala Gly Leu Asp Lys Glu Ala Asp Leu Val
129 340                  345                  350                  355
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131 cac atg gag gtg cgg acc acg gat gga tat gct cac tac ctc acc tgc     1340
132 His Met Glu Val Arg Thr Thr Asp Gly Tyr Ala His Tyr Leu Thr Cys
133             360             365             370
135 agg atc cag gaa tgt gcc gag aca act aga agt ggg cct ttt gcc cgc     1388
136 Arg Ile Gln Glu Cys Ala Glu Thr Thr Arg Ser Gly Pro Phe Ala Arg
137             375             380             385
139 tcc att gac atc agt tcc ctg gtt gtc cag gat gaa tat atc ttc att     1436
140 Ser Ile Asp Ile Ser Ser Leu Val Val Gln Asp Glu Tyr Ile Phe Ile
141             390             395             400
143 cag gta aca act agt gga aga gcc agc tac tac gtg tct tat cga aga     1484
144 Gln Val Thr Thr Ser Gly Arg Ala Ser Tyr Tyr Val Ser Tyr Arg Arg
145      405             410             415
147 gag gcc ttt gct cag ata aag ctg cct aag tac tcg ttg cca aag gac     1532
148 Glu Ala Phe Ala Gln Ile Lys Leu Pro Lys Tyr Ser Leu Pro Lys Asp
149 420             425             430             435
151 atg cac atc atc agt aca gac gag aac caa gta ttt gct gcg gtc caa     1580
152 Met His Ile Ile Ser Thr Asp Glu Asn Gln Val Phe Ala Ala Val Gln
153             440             445             450
155 gaa tgg aac cag aat gac acg tac aac ctc tac atc tca gac acg cgt     1628
156 Glu Trp Asn Gln Asn Asp Thr Tyr Asn Leu Tyr Ile Ser Asp Thr Arg
157             455             460             465
159 ggg att tac ttc act ctg gcc atg gag aac atc aag agc agc aga ggt     1676
160 Gly Ile Tyr Phe Thr Leu Ala Met Glu Asn Ile Lys Ser Ser Arg Gly
161      470             475             480
163 cta atg ggg aac atc att att gaa ttg tat gag gta gca ggt atc aaa     1724
164 Leu Met Gly Asn Ile Ile Ile Glu Leu Tyr Glu Val Ala Gly Ile Lys
165      485             490             495
167 ggg ata ttt ctg gca aac aag aag gtg gac gac cag gtg aag aca tac     1772
168 Gly Ile Phe Leu Ala Asn Lys Lys Val Asp Asp Gln Val Lys Thr Tyr
169 500             505             510             515
171 atc act tac aac aaa ggc agg gat tgg cgc ctg ctg caa gct ccg gat     1820
172 Ile Thr Tyr Asn Lys Gly Arg Asp Trp Arg Leu Leu Gln Ala Pro Asp
173             520             525             530
175 gtg gac ctg aga gga agc cca gtg cac tgc ctg ctg ccc ttc tgt tcc     1868
176 Val Asp Leu Arg Gly Ser Pro Val His Cys Leu Leu Pro Phe Cys Ser
177             535             540             545
179 tta cat ctg cac ctg caa ctc tct gaa aat cca tat tcc tca gga aga     1916
180 Leu His Leu His Leu Gln Leu Ser Glu Asn Pro Tyr Ser Ser Gly Arg
181      550             555             560
183 atc tct agc aag gag aca gcc cca gga ctt gtg gtg gct aca ggc aac     1964
184 Ile Ser Ser Lys Glu Thr Ala Pro Gly Leu Val Val Ala Thr Gly Asn
185      565             570             575
187 att ggc ccg gag ctc tca tat act gat att ggt gtg ttc atc tcc tcc     2012
188 Ile Gly Pro Glu Leu Ser Tyr Thr Asp Ile Gly Val Phe Ile Ser Ser
189 580             585             590             595
191 gat ggg ggc aac aca tgg aga cag atc ttt gat gaa gag tac aat gtc     2060
192 Asp Gly Gly Asn Thr Trp Arg Gln Ile Phe Asp Glu Glu Tyr Asn Val
193             600             605             610
195 tgg ttc cta gac tgg ggt ggt gcc ctc gtg gcc atg aaa cac aca cct     2108
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200 Leu Pro Val Arg His Leu Trp Val Ser Phe Asp Glu Gly His Ser Trp
201         630                 635                 640
203 gac aag tat ggt ttc act tcg gtt cct ctc ttt gtt gac ggg gct ctg     2204
204 Asp Lys Tyr Gly Phe Thr Ser Val Pro Leu Phe Val Asp Gly Ala Leu
205         645                 650                 655
207 gtg gag gca gga atg gag acc cac atc atg aca gtt ttt ggc cac ttc     2252
208 Val Glu Ala Gly Met Glu Thr His Ile Met Thr Val Phe Gly His Phe
209 660                 665                 670                 675
211 agc ctc cgc tcc gaa tgg caa ttg gtg aaa gtg gac tac aaa tct atc     2300
212 Ser Leu Arg Ser Glu Trp Gln Leu Val Lys Val Asp Tyr Lys Ser Ile
213             680                 685                 690
215 ttc agc cgg cat tgc acc aag gag gac tat cag acc tgg cac ctg ctc     2348
216 Phe Ser Arg His Cys Thr Lys Glu Asp Tyr Gln Thr Trp His Leu Leu
217             695                 700                 705
219 aat cag gga gag cct tgt gtc atg gga gaa agg aaa ata ttc aag aaa     2396
220 Asn Gln Gly Glu Pro Cys Val Met Gly Glu Arg Lys Ile Phe Lys Lys
221             710                 715                 720
223 cgt aag cca gga gct cag tgt gcc ctg ggc cga gac cac tca gga tca     2444
224 Arg Lys Pro Gly Ala Gln Cys Ala Leu Gly Arg Asp His Ser Gly Ser
225         725                 730                 735
227 gtg gtc tca gaa ccc tgt gtc tgt gcc aat tgg gac ttc gag tgt gac     2492
228 Val Val Ser Glu Pro Cys Val Cys Ala Asn Trp Asp Phe Glu Cys Asp
229 740                 745                 750                 755
231 tat ggg tat gag aga cat ggg gag agc cag tgt gtc cca gct ttc tgg     2540
232 Tyr Gly Tyr Glu Arg His Gly Glu Ser Gln Cys Val Pro Ala Phe Trp
233             760                 765                 770
235 tac aat cca gca tcc cca tca aag gac tgc agc ctt ggt caa agc tac     2588
236 Tyr Asn Pro Ala Ser Pro Ser Lys Asp Cys Ser Leu Gly Gln Ser Tyr
237             775                 780                 785
239 ctt aac agc act ggg tat cgg cgg att gtg tcc aac aac tgc aca gat     2636
240 Leu Asn Ser Thr Gly Tyr Arg Arg Ile Val Ser Asn Asn Cys Thr Asp
241             790                 795                 800
243 ggg cta agg gag aag tac acc gcc aag gcc cag atg tgc cct gga aaa     2684
244 Gly Leu Arg Glu Lys Tyr Thr Ala Lys Ala Gln Met Cys Pro Gly Lys
245         805                 810                 815
247 gcc cct cgg ggc ctc cat gtg gtg acg acc gat ggg cgg ctg gtg gca     2732
248 Ala Pro Arg Gly Leu His Val Val Thr Thr Asp Gly Arg Leu Val Ala
249 820                 825                 830                 835
251 gag cag ggg cac aat gca act ttc atc atc ctc atg gag gag ggt gat     2780
252 Glu Gln Gly His Asn Ala Thr Phe Ile Ile Leu Met Glu Glu Gly Asp
253             840                 845                 850
255 cta caa agg aca aac atc cag ctt gac ttt ggg gat ggg att gct gtg     2828
256 Leu Gln Arg Thr Asn Ile Gln Leu Asp Phe Gly Asp Gly Ile Ala Val
257             855                 860                 865
259 tcc tac gca aac ttc agc ccc atc gag gac ggc atc aag cac gtg tat     2876
260 Ser Tyr Ala Asn Phe Ser Pro Ile Glu Asp Gly Ile Lys His Val Tyr
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261         870              875              880
263 aag agt gcg ggg atc ttc cag gtg aca gcc tat gca gag aac aac ctt    2924
264 Lys Ser Ala Gly Ile Phe Gln Val Thr Ala Tyr Ala Glu Asn Asn Leu
265     885              890              895
267 ggc tca gac aca gct gtc ctc ttc ctg cat gtg gtt tgt cct gtg gag    2972
268 Gly Ser Asp Thr Ala Val Leu Phe Leu His Val Val Cys Pro Val Glu
269 900              905          '   910    .         915
271 cat gtt cat ctc cga gtt cca ttt gtt gcc ata aga aat aag gag gtc    3020
272 His Val His Leu Arg Val Pro Phe Val Ala Ile Arg Asn Lys Glu Val
273              920              925              930
275 aac atc agt gca gtc gtg tgg ccc agt caa ctg ggg acc ctt acc tat    3068
276 Asn Ile Ser Ala Val Val Trp Pro Ser Gln Leu Gly Thr Leu Thr Tyr
277              935              940              945
279 ttc tgg tgg ttc ggc aat agc aca aag cct ctc atc act ttg gac agc    3116
280 Phe Trp Trp Phe Gly Asn Ser Thr Lys Pro Leu Ile Thr Leu Asp Ser
281              950              955              960
283 agc att tcc ttc aca ttc ctt gca gaa gga acc gac acc atc aca gtc    3164
284 Ser Ile Ser Phe Thr Phe Leu Ala Glu Gly Thr Asp Thr Ile Thr Val
285     965         .        970      '. .   .: 975       ,   .
287 cag gtg gct gct ggg aat gcc ctc atc cag gac aca aaa gag att gca    3212
288 Gln Val Ala Ala Gly Asn Ala Leu Ile Gln Asp Thr Lys Glu Ile Ala
289 980              985              990              995
291 gtt cat gaa tat ttc   cag tcc cag ctt tta   tca ttc tct cct aat    3257
292 Val His Glu Tyr Phe   Gln Ser Gln Leu Leu   Ser Phe Ser Pro Asn
293              1000             1005             1010
295 ctg gat tac cac aat   cct gac att cct gag   tgg aga aaa gat att    3302
296 Leu Asp Tyr His Asn   Pro Asp Ile Pro Glu   Trp Arg Lys Asp Ile
297              1015             1020             1025
299 ggc aat gtc atc aag   cga gct ctg gtt aaa   gta acc agt gtc cca    3347
300 Gly Asn Val Ile Lys   Arg Ala Leu Val Lys   Val Thr Ser Val Pro
301              1030             1035             1040
303 gag gac cag atc ctc   att gcc gtg ttt cct   ggt ctc ccc act tca    3392
304 Glu Asp Gln Ile Leu   Ile Ala Val Phe Pro   Gly Leu Pro Thr Ser
305              1045             1050             1055
307 gca gag ctt ttc att   ctt cca ccc aag aac   ctg aca gag agg agg    3437
308 Ala Glu Leu Phe Ile   Leu Pro Pro Lys Asn   Leu Thr Glu Arg Arg
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311 aaa ggc aat gaa ggg   gac ctg gaa caa att   gta gaa aca ctg ttt    3482
312 Lys Gly Asn Glu Gly   Asp Leu Glu Gln Ile   Val Glu Thr Leu Phe
313              1075             1080             1085
315 aat gct ctc aac caa   aat ttg gtc cag ttt   gag ctg aag ccg ggg    3527
316 Asn Ala Leu Asn Gln   Asn Leu Val Gln Phe   Glu Leu Lys Pro Gly
317              1090             1095             1100
319 gta caa gtc att gtg   tat gtc aca cag ctg   acg tta gct cca ttg    3572
320 Val Gln Val Ile Val   Tyr Val Thr Gln Leu   Thr Leu Ala Pro Leu
321              1105             1110             1115
323 gtg gac tcc agt gct   ggg cac agc agc tca   gcc atg ctt atg cta    3617
324 Val Asp Ser Ser Ala   Gly His Ser Ser Ser   Ala Met Leu Met Leu
325              1120             1125             1130
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VERIFICATION SUMMARY   DATE: 08/17/2006
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